

0/506630

## SEQUENCE LISTING

<110> GOKHALE, Rajesh  
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WU, Nicholas  
CANE, David

<120> METHODS TO MEDIATE POLYKETIDE SYNTHASE  
MODULE EFFECTIVENESS

<130> 300622004601

<140> US 10/506,630  
<141> 2002-03-04

<150> PCT/US03/06910  
<151> 2002-03-04

<150> US 10/091,244  
<151> 2002-03-04

<150> 60/361,758  
<151> 2002-03-04

<160> 41

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<220>  
<223> Nhe site upstream of the KS at position 7570

<400> 1  
gctagcgagc cgatc

15

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<223> Nhe site upstream of the KS at position 28710

<400> 2  
gctagcgacc cgatc

15

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<223> N-terminal linker of M3

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Met Thr Asp Ser Glu Lys Val Ala Glu Tyr Leu Arg Arg Ala Thr Leu  
1 5 10 15  
Asp Leu Arg Ala Ala Arg Gln Arg Ile Arg Glu Leu Glu Ser Asp  
20 25 30

<210> 4  
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<220>  
<223> Primer

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actagtaggc tgttcgcggc ctcac

25

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<220>  
<223> Primer

<400> 5  
gggaattcag gtcctctccc ccgc

24

<210> 6  
<211> 23  
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<220>  
<223> Primer

<400> 6  
ccatatggtg gtcgaccggc tcg

23

<210> 7  
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<220>  
<223> primer

<400> 7  
gaattcctac aggtcctctc cccc

24

<210> 8  
<211> 22  
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<220>  
<223> primer

<400> 8  
ccatatgctg cgcgaccggc tg

22

<210> 9  
<211> 25  
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<220>  
<223> primer

<400> 9  
gaattctcaa tcgccgtcga gctcc

25

<210> 10  
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ccatatggtg gtcgaccggc tcg.

23

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<220>  
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<400> 11  
actagtgagg aaaccggcga ccg

23

<210> 12  
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<400> 12  
ccatatgctg cgcgaccggc tg

22

<210> 13  
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<212> DNA  
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<220>  
<223> primer

<400> 13

gaattcttag ccgagct~~cc~~ cgtc

24

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<223> primer

<400> 14  
ccatatggtg gtcgaccggc tcg

23

<210> 15  
<211> 27  
<212> DNA  
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<220>  
<223> primer

<400> 15  
gaattcttag aacagcctgt cccgcag

27

<210> 16  
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<220>  
<223> primer

<400> 16  
ctgctcgaga ggctgttcgc ggccta

27

<210> 17  
<211> 27  
<212> DNA  
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<220>  
<223> primer

<400> 17  
cccgctgagc ctacaggtcc tctcccc

27

<210> 18  
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<212> PRT  
<213> Artificial Sequence

<220>  
<223> Intra-polypeptide linker

<400> 18  
Gly Gly Ala Thr Gly Ala Glu Gln Ala Ala Pro Ala Thr Thr Ala Pro  
1 5 10 15

Val Asp

<210> 19  
<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Intra-polypeptide linker

<400> 19  
Val Gly Asp Ala Asp Gln Ala Ala Val Arg Val Val Gly Ala Ala Asp  
1 5 10 15  
Glu Ser

<210> 20  
<211> 21  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Intra-polypeptide linker

<400> 20  
Val Gly Ala Ala Glu Ala Glu Gln Ala Pro Ala Leu Val Arg Glu Val  
1 5 10 15  
Pro Lys Asp Ala Asp  
20

<210> 21  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Intra-polypeptide linker

<400> 21  
Phe Gly Ser Ala Ala Asn Arg Pro Ala Glu Ile Gly Thr Ala Ala Ala  
1 5 10 15  
Glu

<210> 22  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Intra-polypeptide linker

<400> 22  
Leu Gly Glu Arg Pro Ala Ala Pro Ala Pro Val Thr Arg Asp Val Ser  
1 5 10 15  
Asp

<210> 23  
<211> 19  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Intra-polypeptide linker

<400> 23  
Gly Glu Thr Val Ala Gly Ala Pro Ala Thr Pro Val Thr Thr Val Ala  
1 5 10 15  
Asp Ala Gly

<210> 24  
<211> 21  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Intra-polypeptide linker

<400> 24  
Glu Leu Phe Thr Gly Glu Asn Pro Ala Pro Val Arg Gly Pro Val Ser  
1 5 10 15  
Ala Val Gly Gln Asp  
20

<210> 25  
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<212> PRT  
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<220>  
<223> Intra-polypeptide linker

<400> 25  
Glu Leu Phe Thr Gly Glu Asn Pro Ala Pro Val Arg Gly Pro Val Ser  
1 5 10 15  
Val Val Gly Gln Asp  
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<210> 26  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Intra-polypeptide linker

<400> 26  
Glu Leu Phe Thr Gly Glu Asn Pro Ala Pro Val Arg Gly Pro Val Ser  
1 5 10 15  
Ala Gly Gln Asp  
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<210> 27

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> N-Terminal Inter-polypeptide linker

<400> 27

Val Thr Asp Ser Glu Lys Val Ala Glu Tyr Leu Arg Arg Ala Thr Leu  
1 5 10 15  
Asp Leu Arg Ala Ala Arg Gln Arg Ile Arg Glu Leu Glu Ser  
20 25 30

<210> 28

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> N-Terminal Inter-polypeptide linker

<400> 28

Met Ser Gly Asp Asn Gly Met Thr Glu Glu Lys Leu Arg Arg Tyr Leu  
1 5 10 15  
Lys Arg Thr Val Thr Glu Leu Asp Ser Val Thr Ala Arg Leu Arg Glu  
20 25 30  
Val Glu His Arg Ala Gly  
35

<210> 29

<211> 34

<212> PRT

<213> Artificial Sequence

<220>

<223> N-Terminal Inter-polypeptide linker

<400> 29

Met Ser Ala Pro Asn Glu Gln Ile Val Asp Ala Leu Arg Ala Ser Leu  
1 5 10 15  
Lys Glu Asn Val Arg Leu Gln Gln Glu Asn Ser Ala Leu Ala Ala Ala  
20 25 30  
Ala Ala

<210> 30

<211> 34

<212> PRT

<213> Artificial Sequence

<220>

<223> N-Terminal Inter-polypeptide linker

<400> 30

Val Ser Ala Ser Tyr Glu Lys Val Val Glu Ala Leu Arg Lys Ser Leu  
1 5 10 15  
Glu Glu Val Gly Thr Leu Lys Lys Arg Asn Arg Gln Leu Ala Asp Ala  
20 25 30  
Ala Gly

<210> 31  
<211> 33  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> N-Terminal Inter-polypeptide linker

<400> 31  
Val Ala Asp Glu Gly Gln Leu Arg Asp Tyr Leu Lys Arg Ala Ile Ala  
1 5 10 15  
Asp Ala Arg Asp Ala Arg Thr Arg Leu Arg Glu Val Glu Glu Gln Ala  
20 25 30  
Arg

<210> 32  
<211> 30  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> N-Terminal Inter-polypeptide linker

<400> 32  
Met Ala Thr Asp Glu Lys Leu Leu Lys Tyr Leu Lys Arg Val Thr Ala  
1 5 10 15  
Glu Leu His Ser Leu Arg Lys Gln Gly Ala Arg His Ala Asp  
20 25 30

<210> 33  
<211> 32  
<212> PRT  
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<220>  
<223> N-Terminal Inter-polypeptide linker

<400> 33  
Met Arg Glu Asp Gln Leu Leu Asp Ala Leu Arg Lys Ser Val Lys Glu  
1 5 10 15  
Asn Ala Arg Leu Arg Lys Ala Asn Thr Ser Leu Arg Ala Ala Met Asp  
20 25 30

<210> 34  
<211> 33  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> N-Terminal Inter-polypeptide linker

<400> 34  
Met Pro Glu Gln Asp Lys Val Val Glu Tyr Leu Arg Trp Ala Thr Ala  
1 5 10 15  
Glu Leu His Thr Thr Arg Ala Lys Leu Glu Ala Leu Ala Ala Asn

Thr

<210> 35  
 <211> 388  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Alignment of the EryA SU

<400> 35  
 Val Val Phe Val Phe Pro Gly Gln Gly Ala Gln Trp Ala Gly Met Ala  
 1 5 10 15  
 Gly Glu Leu Ile Gly Glu Ser Arg Val Phe Ala Ala Ala Met Asp Ala  
 20 25 30  
 Cys Ala Arg Ala Phe Glu Pro Val Thr Asp Trp Thr Leu Ala Gln Val  
 35 40 45  
 Leu Asp Ser Pro Glu Gln Ser Arg Arg Val Glu Val Val Gln Pro Ala  
 50 55 60  
 Leu Phe Ala Val Gln Thr Ser Leu Ala Ala Leu Trp Arg Ser Phe Gly  
 65 70 75 80  
 Val Thr Pro Asp Ala Val Val Gly His Ser Ile Gly Glu Leu Ala Ala  
 85 90 95  
 Ala His Val Cys Gly Ala Ala Gly Ala Ala Asp Ala Ala Arg Ala Ala  
 100 105 110  
 Ala Leu Trp Ser Arg Glu Met Ile Pro Ile Val Gly Asn Gly Asp Met  
 115 120 125  
 Met Ala Val Ala Leu Ser Ala Asp Glu Ile Glu Pro Arg Ile Ala Arg  
 130 135 140  
 Trp Asp Asp Val Val Leu Ala Gly Val Asn Gly Pro Arg Ser Val Leu  
 145 150 155 160  
 Leu Thr Gly Ser Pro Glu Pro Val Ala Arg Arg Val Gln Glu Leu Ser  
 165 170 175  
 Ala Glu Gly Val Arg Ala Gln Val Ile Asn Val Ser Met Ala Ala His  
 180 185 190  
 Ser Ala Gln Val Asp Asp Ile Ala Glu Gly Met Arg Ser Ala Leu Ala  
 195 200 205  
 Trp Phe Ala Pro Gly Gly Ser Glu Val Pro Phe Tyr Ala Ser Leu Thr  
 210 215 220  
 Gly Gly Ala Val Asp Thr Arg Glu Leu Val Ala Asp Tyr Trp Arg Arg  
 225 230 235 240  
 Ser Phe Arg Leu Pro Val Arg Phe Asp Glu Ala Ile Arg Ser Ala Leu  
 245 250 255  
 Glu Val Gly Pro Gly Thr Phe Val Glu Ala Ser Pro His Pro Val Ile  
 260 265 270  
 Ala Ala Ala Leu Gln Gln Thr Leu Asp Ala Glu Gly Ser Ser Ala Ala  
 275 280 285  
 Val Val Pro Thr Leu Gln Arg Gly Gln Gly Gly Met Arg Arg Phe Leu  
 290 295 300  
 Leu Ala Ala Ala Gln Ala Phe Thr Gly Gly Val Ala Val Asp Trp Thr  
 305 310 315 320  
 Ala Ala Tyr Asp Asp Val Gly Pro Asn Pro Ala Leu Gly Arg Glu Ala  
 325 330 335  
 Asp Ala Glu Ala Thr Phe Arg Glu Leu Gly Leu Asp Ser Val Leu Ala  
 340 345 350  
 Ala Gln Ile Arg Ala Lys Val Ser Ala Ala Ile Gly Arg Glu Val Asn  
 355 360 365  
 Ile Ala Leu Leu Tyr Asp His Pro Thr Pro Arg Ala Leu Ala Glu Ala  
 370 375 380  
 Leu Ala Ala Gly

<210> 36  
 <211> 1397  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Alignment of the EryA SU

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 Ala Ala Pro Gly Glu Pro Val Ala Val Val Ala Met Ala Cys Arg Leu  
 1 5 10 15  
 Pro Gly Gly Val Ser Thr Pro Glu Glu Phe Trp Glu Leu Leu Ser Glu  
 20 25 30  
 Gly Arg Asp Ala Val Ala Gly Leu Pro Thr Asp Arg Gly Trp Asp Leu  
 35 40 45  
 Asp Ser Leu Phe His Pro Asp Pro Thr Arg Ser Gly Thr Ala His Gln  
 50 55 60  
 Arg Gly Gly Gly Phe Leu Thr Glu Ala Thr Ala Phe Asp Pro Ala Phe  
 65 70 75 80  
 Phe Gly Met Ser Pro Arg Glu Ala Leu Ala Val Asp Pro Gln Gln Arg  
 85 90 95  
 Leu Met Leu Glu Leu Ser Trp Glu Val Leu Glu Arg Ala Gly Ile Pro  
 100 105 110  
 Pro Thr Ser Ile Gln Ala Ser Pro Thr Gly Val Phe Val Gly Leu Ile  
 115 120 125  
 Pro Gln Glu Tyr Gly Pro Arg Leu Ala Glu Gly Gly Glu Gly Val Glu  
 130 135 140  
 Gly Tyr Leu Met Thr Gly Thr Thr Ser Val Ala Ser Gly Arg Ile  
 145 150 155 160  
 Ala Tyr Thr Leu Gly Leu Glu Gly Pro Ala Ile Ser Val Asp Thr Ala  
 165 170 175  
 Cys Ser Ser Ser Leu Val Ala Val His Leu Ala Cys Gln Ser Leu Arg  
 180 185 190  
 Arg Gly Glu Ser Ser Ile Ala Met Ala Gly Gly Val Thr Val Met Pro  
 195 200 205  
 Thr Pro Gly Met Leu Val Asp Phe Ser Arg Met Asn Ser Leu Ala Pro  
 210 215 220  
 Asp Gly Arg Cys Lys Ala Phe Ser Ala Gly Ala Asn Gly Phe Gly Met  
 225 230 235 240  
 Ala Glu Gly Ala Gly Met Leu Leu Ile Glu Arg Leu Ser Asp Ala Arg  
 245 250 255  
 Arg Asn Gly His Pro Val Leu Ala Val Leu Arg Gly Thr Ala Val Asn  
 260 265 270  
 Ser Asp Gly Ala Ser Asn Gly Leu Ser Ala Pro Asn Gly Arg Ala Gln  
 275 280 285  
 Val Arg Val Ile Gln Gln Ala Leu Ala Glu Ser Gly Leu Gly Pro Ala  
 290 295 300  
 Asp Ile Asp Ala Val Glu Ala His Gly Thr Gly Thr Arg Leu Gly Asp  
 305 310 315 320  
 Pro Ile Glu Ala Arg Ala Leu Phe Glu Ala Tyr Gly Arg Asp Arg Glu  
 325 330 335  
 Gln Pro Leu His Leu Gly Ser Val Lys Ser Asn Leu Gly His Thr Gln  
 340 345 350  
 Ala Ala Ala Gly Val Ala Gly Val Ile Lys Met Val Leu Ala Met Arg  
 355 360 365  
 Ala Gly Thr Leu Pro Arg Thr Leu His Ala Ser Glu Arg Ser Lys Glu  
 370 375 380  
 Ile Asp Trp Ser Ser Gly Ala Ile Ser Leu Ile Asp Glu Pro Glu Pro  
 385 390 395 400

Trp Pro Ala Gly Ala Arg Pro Arg Arg Ala Gly Val Ser Ser Phe Gly  
 405 410 415  
 Ile Ser Gly Thr Asn Ala His Ala Ile Ile Glu Glu Ala Pro Gln Val  
 420 425 430  
 Val Glu Gly Glu Arg Val Glu Ala Gly Asp Val Val Ala Pro Trp Val  
 435 440 445  
 Leu Ser Ala Ser Ser Ala Glu Gly Leu Arg Ala Gln Ala Ala Arg Leu  
 450 455 460  
 Ala Ala His Leu Arg Glu His Pro Gly Gln Asp Pro Arg Asp Ile Ala  
 465 470 475 480  
 Tyr Ser Leu Ala Thr Gly Arg Ala Ala Leu Pro His Arg Ala Ala Phe  
 485 490 495  
 Ala Pro Val Asp Glu Ser Ala Ala Leu Arg Val Leu Asp Gly Leu Ala  
 500 505 510  
 Thr Gly Asn Ala Asp Gly Ala Ala Val Gly Thr Ser Arg Ala Gln Gln  
 515 520 525  
 Arg Ala Val Phe Val Trp Ala Ala Val Asp Asp Thr Ser Pro Ala Ala  
 530 535 540  
 Leu Arg Glu Ala Asp Ala Leu Glu Pro His Leu Asp Arg Glu Val Ile  
 545 550 555 560  
 Pro Phe Leu Arg Ala Glu Ala Ala Arg Arg Glu Gln Asp Ala Ala Leu  
 565 570 575  
 Ser Thr Glu Asp Val Val Met Ala Val Met Val Ser Met Arg Ala His  
 580 585 590  
 Val Glu Ala Ile Gln Ile Cys Ala Ala Leu Ser Leu Asp Asp Ala Ala  
 595 600 605  
 Arg Val Val Ala Leu Arg Ser Arg Val Ile Ala Thr Met Pro Gly Asn  
 610 615 620  
 Lys Gly Ala Ser Ile Ala Ala Pro Ala Gly Glu Val Arg Ala Arg Ile  
 625 630 635 640  
 Gly Asp Arg Val Glu Ile Ala Gly Arg Ser Val Val Val Ala Asp Ser  
 645 650 655  
 Asp Glu Leu Asp Arg Leu Val Ala Ser Cys Thr Thr Glu Cys Ile Arg  
 660 665 670  
 Ala Lys Arg Leu Ala Asp Tyr Ser Ser Ser His Val Glu Thr Ile Arg  
 675 680 685  
 Asp Ala Leu His Ala Glu Leu Gly Glu Asp Phe His Pro Leu Pro Gly  
 690 695 700  
 Phe Val Pro Phe Phe Thr Val Thr Gly Arg Trp Thr Gln Pro Asp Glu  
 705 710 715 720  
 Leu Asp Ala Gly Tyr Arg Asn Ile Arg Thr Arg Ala Asp Val Arg Ala  
 725 730 735  
 Leu Ala Glu Gln Tyr Arg Thr Leu Val Ala Ile Leu Thr Ala Ala Ile  
 740 745 750  
 Glu Glu Ile Gly Asp Gly Ser Gly Ala Asp Leu Ser Ala Ile His Ser  
 755 760 765  
 Arg Gly Asp Gly Ser Leu Ala Asp Phe Gly Glu Ala Leu Ser Arg Phe  
 770 775 780  
 Ala Ala Ala Val Asp Trp Glu Ser Val His Leu Gly Thr Gly Ala Arg  
 785 790 795 800  
 Arg Val Pro Leu Pro Thr Tyr Pro Phe Gln Arg Glu Arg Val Trp Leu  
 805 810 815  
 Glu Pro Lys Pro Val Ala Arg Arg Ser Thr Glu Val Asp Glu Val Ser  
 820 825 830  
 Ala Leu Arg Tyr Arg Ile Glu Trp Arg Pro Thr Gly Ala Gly Glu Pro  
 835 840 845  
 Ala Arg Leu Asp Gly Thr Trp Leu Val Ala Lys Tyr Ala Gly Thr Ala  
 850 855 860  
 Asp Glu Thr Ser Thr Ala Ala Arg Glu Ala Leu Glu Ser Ala Gly Ala  
 865 870 875 880  
 Arg Val Arg Glu Leu Val Val Asp Ala Arg Cys Gly Arg Asp Glu Leu  
 885 890 895

Ala Glu Arg Leu Arg Ser Val Gly Glu Val Ala Gly Val D Ser Leu  
 900 905 910

Leu Ala Val Asp Glu Ala Glu Pro Glu Glu Ala Pro Leu Ala Leu Ala  
 915 920 925

Ser Leu Ala Asp Thr Leu Ser Leu Val Gln Ala Met Val Ser Ala Glu  
 930 935 940

Leu Gly Cys Pro Leu Trp Thr Val Thr Glu Ser Ala Val Ala Thr Gly  
 945 950 955 960

Pro Phe Glu Arg Val Arg Asn Ala Ala His Gly Ala Leu Trp Gly Val  
 965 970 975

Gly Arg Val Ile Ala Leu Glu Asn Pro Ala Val Trp Gly Gly Leu Val  
 980 985 990

Asp Val Pro Ala Gly Ser Val Ala Glu Leu Ala Arg His Leu Ala Ala  
 995 1000 1005

Val Val Ser Gly Gly Ala Gly Glu Asp Gln Leu Ala Leu Arg Ala Asp  
 1010 1015 1020

Gly Val Tyr Gly Arg Arg Trp Val Arg Ala Ala Pro Ala Thr Asp  
 1025 1030 1035 1040

Asp Glu Trp Lys Pro Thr Gly Thr Val Leu Val Thr Gly Gly Thr Gly  
 1045 1050 1055

Gly Val Gly Gly Gln Ile Ala Arg Trp Ile Ala Arg Pro Gly Ala Pro  
 1060 1065 1070

His Leu Leu Leu Val Ser Arg Ser Gly Pro Asp Ala Asp Gly Ala Gly  
 1075 1080 1085

Glu Leu Val Ala Glu Leu Glu Ala Leu Gly Ala Arg Thr Thr Val Ala  
 1090 1095 1100

Ala Cys Asp Val Ile Asp Arg Glu Ser Val Arg Glu Leu Leu Gly Gly  
 1105 1110 1115 1120

Ile Gly Asp Asp Val Pro Leu Ser Ala Val Phe His Ala Ala Ala Thr  
 1125 1130 1135

Leu Asp Asp Gly Thr Val Asp Thr Leu Thr Gly Glu Arg Ile Glu Arg  
 1140 1145 1150

Ala Ser Arg Ala Lys Val Leu Gly Ala Arg Asn Leu His Glu Leu Thr  
 1155 1160 1165

Arg Glu Leu Asp Leu Thr Ala His Val Leu Phe Ser Ser Phe Ala Ser  
 1170 1175 1180

Ala Phe Gly Ala Pro Gly Leu Gly Gly Tyr Ala Pro Gly Asn Ala Tyr  
 1185 1190 1195 1200

Leu Asp Gly Leu Ala Gln Gln Arg Arg Ser Asp Gly Leu Pro Ala Thr  
 1205 1210 1215

Ala Val Ala Trp Gly Thr Trp Ala Gly Ser Gly Met Ala Glu Gly Ala  
 1220 1225 1230

Val Ala Asp Arg Phe Arg Arg His Gly Val Ile Glu Met Pro Pro Glu  
 1235 1240 1245

Thr Ala Cys Arg Ala Leu Gln Asn Ala Leu Asp Arg Ala Glu Val Cys  
 1250 1255 1260

Pro Ile Val Ile Asp Val Arg Trp Asp Arg Phe Leu Leu Ala Tyr Thr  
 1265 1270 1275 1280

Ala Gln Arg Pro Thr Arg Leu Phe Asp Glu Ile Asp Asp Ala Arg Arg  
 1285 1290 1295

Ala Ala Pro Gln Ala Pro Ala Glu Pro Arg Val Gly Ala Leu Ala Ser  
 1300 1305 1310

Leu Pro Ala Pro Glu Arg Glu Glu Ala Leu Phe Glu Leu Val Arg Ser  
 1315 1320 1325

His Ala Ala Ala Val Leu Gly His Ala Ser Ala Glu Arg Val Pro Ala  
 1330 1335 1340

Asp Gln Ala Ala Glu Val Leu Ser Leu Glu Asn Arg Leu Gly Ala Ala  
 1345 1350 1355 1360

Thr Val Arg Leu Pro Thr Thr Val Phe Asp Asp Val Arg Thr Leu  
 1365 1370 1375

Ala His Leu Ala Ala Glu Leu Gly Gly Ala Thr Gly Ala Glu Gln Ala  
 1380 1385 1390

Ala Pro Ala Thr Thr  
1395

<210> 37  
<211> 1114  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Alignment of the EryA SU

<400> 37  
Ala Pro Val Asp Glu Ile Ile Gly Met Ala Leu Glu Val Asp Ser Glu  
1 5 10 15  
Arg Leu Glu Leu Ile Thr Ser Gly Arg Asp Ser Ala Ala Glu Val Asp  
20 25 30  
Val Pro Asp Glu Leu Met Ala Ser Asp Ala Ala Gly Thr Arg Ala His  
35 40 45  
Asn Phe Met Ala Gly Gly Asp Ala Ala Ile Ser Leu Met Gln Ala Thr  
50 55 60  
Thr Ala Leu Ser Ile Pro Glu Thr Arg Gly Ser Asp Val Met Ser His  
65 70 75 80  
Gln Gly Ala Thr Gly Arg Pro Arg Pro Glu Asp Gly Val Asp Leu Leu  
85 90 95  
Thr Asn Thr Ala Ser Ala Ile Ala Val Leu Leu Ala Leu Thr Ser Val  
100 105 110  
Ala Leu Thr Cys Gly Ser Asp Gly Asp Gln Gly Leu Val Ala Val Ser  
115 120 125  
Ala Gly Glu Val Phe Thr Glu Ser Arg Gln Gly Ala Ser Pro Cys Pro  
130 135 140  
Ser Asp Glu Asp Gly Leu Gly Ser Ala Phe Val Val Gln Arg Asp Arg  
145 150 155 160  
Glu Arg Arg Gly Val Val Ala Ser Val Gln Ser Ser Val Ala Gln Arg  
165 170 175  
Arg Trp Ala Arg Ala Ile Thr Gly Ala Val Ala Val Arg Val Ala Ser  
180 185 190  
Leu Ala Thr Lys Ser Gly Ser Ser Gly Val Leu Leu Ser Ile Ala Val  
195 200 205  
Ala Ile Val Ile Gly Leu Glu Arg Val Val Pro Met Cys Arg Gly Arg  
210 215 220  
Ser Gly Leu Ile Asp Ser Ser Glu Ile Glu Leu Ala Asp Gly Val Arg  
225 230 235 240  
Glu Ser Pro Ala Ala Asp Gly Val Gly Ala Val Val Ile Ala Pro Glu  
245 250 255  
Pro Glu Pro Val Pro Gln Pro Arg Arg Met Leu Pro Ala Thr Gly Val  
260 265 270  
Val Val Val Leu Ala Arg Thr Gly Ala Ala Leu Arg Gly Arg Leu Ala  
275 280 285  
Asp His Leu Ala Ala His Pro Gly Ile Ala Pro Ala Asp Val Ser Trp  
290 295 300  
Thr Met Arg Ala Gln His Phe Glu Glu Ala Val Leu Ala Ala Asp Thr  
305 310 315 320  
Ala Glu Ala Val His Arg Arg Ala Val Asp Ala Val Val Pro Gly Val  
325 330 335  
Val Thr Gly Ser Ala Ser Asp Gly Gly Ser Val Phe Val Ala Glu Ala  
340 345 350  
Arg Glu Pro Val Pro Glu Ser Ile Ala Glu Asp Ala Val Leu Ser Glu  
355 360 365  
Val Ala Gly Arg Ser Val Ser Glu Val Leu Glu Pro Arg Pro Asp Ala  
370 375 380  
Pro Ser Leu Glu Asp Val Val Leu Ala Val Met Val Arg Leu Arg Ala

385	390	395	400
Cys Ala Val Ser Ile Gln Ile Val Ala Ala		Leu Ser Leu Glu Asp Gly	
405		410	415
Met Arg Val Val Ala Arg Arg Ser Arg Ala	Val Arg Ala Val Ala Gly		
420	425	430	
Arg Gly Ser Leu Ser Val Arg Gly Gly Arg	Ser Asp Val Glu Lys Leu		
435	440	445	
Leu Ala Asp Asp Ser Trp Thr Gly Arg Leu	Glu Val Ala Gly Asp Ala		
450	455	460	
Val Val Val Ala Asp Ala Gln Ala Ala Arg	Glu Phe Leu Glu Tyr Cys		
465	470	475	480
Glu Gly Val Gly Ile Arg Ala Arg Ala Ile	Pro Asp Tyr Ser Thr Ala		
485	490	495	
His Val Glu Pro Val Arg Asp Glu Leu Val	Gln Ala Leu Ala Gly Ile		
500	505	510	
Thr Pro Arg Arg Ala Glu Val Pro Phe Phe	Thr Leu Thr Gly Asp Phe		
515	520	525	
Leu Asp Gly Thr Glu Leu Asp Ala Gly Tyr	Arg Asn Ile His Pro Glu		
530	535	540	
His Ser Val Gln Ala Leu Thr Asp Gln Tyr	Ala Thr Ile Val Pro Val		
545	550	555	560
Leu Ala Ser Ser Val Gln Glu Thr Leu Asp	Asp Ala Glu Ser Asp Ala		
565	570	575	
Ala Val Leu Gly Thr Glu Asp Ala Gly Asp	Ala Asp Arg Phe Leu Thr		
580	585	590	
Ala Leu Ala Asp His Thr Arg Ala Val Asp	Trp Glu Ala Val Leu Gly		
595	600	605	
Arg Ala Gly Leu Val Asp Gly Gln Gly Lys	Phe Leu Leu Pro Asp Arg		
610	615	620	
Thr Thr Pro Arg Glu Leu Asp Gly Trp Phe	Arg Val Asp Thr Glu Val		
625	630	635	640
Pro Arg Ser Glu Pro Ala Ala Leu Arg Gly	Arg Trp Val Val Val Pro		
645	650	655	
Glu Gly His Glu Glu Asp Gly Trp Thr Val	Glu Val Arg Ser Ala Leu		
660	665	670	
Ala Glu Ala Ala Glu Pro Glu Val Thr Arg	Gly Val Gly Gly Leu Val		
675	680	685	
Gly Asp Cys Ala Gly Val Leu Ala Leu Glu	Gly Asp Gly Ala Val		
690	695	700	
Gln Thr Leu Val Val Arg Glu Leu Asp Ala	Glu Gly Ile Asp Ala Pro		
705	710	715	720
Leu Trp Thr Val Phe Gly Asp Ala Gly Ser	Pro Val Ala Arg Pro Asp		
725	730	735	
Gln Ala Lys Leu Trp Leu Gly Gln Val Ala	Ser Leu Arg Gly Pro Arg		
740	745	750	
Trp Thr Gly Leu Val Leu Pro His Met Pro	Asp Pro Glu Leu Arg Gly		
755	760	765	
Arg Leu Thr Val Leu Ala Gly Ser Glu Asp	Gln Val Val Ala Asp Ala		
770	775	780	
Val Arg Ala Arg Leu Ser Pro Ala His Val	Thr Ala Thr Ser Glu Tyr		
785	790	795	800
Ala Val Gly Ile Val Gly Thr Ala Gly Leu	Ala Glu Val Ala Trp Ala		
805	810	815	
Gly Arg Ala Glu His Ala Val Ser Arg Arg	Gly Pro Asp Thr Glu Gly		
820	825	830	
Val Gly Asp Thr Ala Glu Leu Thr Asp Leu	Ala Arg Val Ser Val His		
835	840	845	
Cys Val Ser Ser Arg Glu Pro Val Arg Glu	Ile Val His Gly Leu Ile		
850	855	860	
Glu Gln Gly Asp Val Val Arg Gly Val Val	Ala Ala Gly Leu Pro Gln		
865	870	875	880
Gln Val Ala Ile Asn Asp Met Asp Glu Ala	Ala Phe Asp Glu Val Val		

885 890 895

Ala Ala Ala Gly Gly Ala Val His Asp Leu Cys Ser Asp Ala Glu Leu  
 900 905 910  
 His Leu Ile Phe Gly Gly Val Trp Gly Ser Ala Arg Gln Gly Ala Ala  
 915 920 925  
 Ala Gly Asn Ala Phe Asp Ala Phe Arg His Arg Gly Arg Leu Pro Ala  
 930 935 940  
 Thr Ser Val Ala Gly Leu Ala Gly Gly Met Thr Gly Asp Glu Glu Ala  
 945 950 955 960  
 Val Ser Phe Leu Arg Glu Arg Val Arg Ala Met Pro Val Pro Arg Leu  
 965 970 975  
 Ala Ala Leu Asp Arg Val Ala Ser Gly Glu Thr Ala Val Val Val Thr  
 980 985 990  
 Asp Val Asp Trp Pro Ala Phe Ala Glu Ser Tyr Thr Ala Arg Pro Arg  
 995 1000 1005  
 Pro Leu Leu Asp Arg Ile Val Thr Thr Ala Pro Ser Glu Arg Ala Gly  
 1010 1015 1020  
 Glu Pro Glu Thr Glu Ser Leu Arg Asp Arg Leu Gly Leu Pro Arg Ala  
 1025 1030 1035 1040  
 Glu Arg Thr Ala Glu Val Arg Leu Val Arg Thr Ser Thr Thr Val Leu  
 1045 1050 1055  
 His Asp Asp Pro Lys Ala Val Arg Ala Thr Thr Pro Lys Glu Phe Leu  
 1060 1065 1070  
 Ala Val Arg Asn Leu Leu Asn Ala Ala Thr Leu Arg Leu Pro Ser Thr  
 1075 1080 1085  
 Leu Val Phe Asp Asn Ala Ser Ala Val Gly Phe Leu Asp Ala Glu Gly  
 1090 1095 1100  
 Thr Glu Val Arg Gly Glu Ala Pro Ser Ala  
 1105 1110

<210> 38  
 <211> 1128  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Alignment of the EryA SU

<400> 38  
 Glu Leu Glu Ser Asp Ile Ile Ser Met Ala Leu Gly Val Asn Thr Gln  
 1 5 10 15  
 Arg Ile Glu Leu Leu Arg Glu Gly Gly Glu Thr Leu Ser Gly Phe Thr  
 20 25 30  
 Asp Leu Ala Arg Leu His His Pro Asp Pro Asp Asn Pro Gly Thr Ser  
 35 40 45  
 Tyr Val Asp Lys Gly Phe Leu Asp Asp Ala Gly Ala Glu Val Ser Ala  
 50 55 60  
 Met Leu Ile Thr Ser Leu Val Asn Ile Asp His Ser Arg Gly Thr Ala  
 65 70 75 80  
 Leu Val Ala Lys Phe Gly Gly Glu Asp Thr Ala Ala Ala Glu Asp Val  
 85 90 95  
 Glu Ser Val Thr Val Ala Pro Ala Ala Ile Ser Thr Met Leu Ser Ile  
 100 105 110  
 Ser Ser Val Ala Leu Ile Val Glu Ser Lys Gly Glu Ser Ser Met Val  
 115 120 125  
 Val Ala Ala Ala Thr Gly Val Phe Val Asp Ser Arg Gln Arg Ala Ala  
 130 135 140  
 Ala Ser Ala Gly Ala Gly Asp Gly Phe Ser Val Thr Leu Val Leu Glu  
 145 150 155 160  
 Arg Glu Arg Asn His Glu Ala Val Val Arg Ser Ile Gln Ser Ser Pro  
 165 170 175

Ala Arg Arg Gln Leu Glu Ser Cys Leu Glu Pro Gly Val Asp Ala Ala  
 180 185 190  
 Ile Ala Asn Leu Asp Thr Arg Asp Asp Ala Asp Arg Leu Trp Leu Ser  
 195 200 205  
 Ile Thr Val Thr Leu Val Val Ala Leu Arg Asn Glu Leu Ala Thr His  
 210 215 220  
 Val Glu Pro Thr Pro His Val Asp Ser Ser Gly Val Ala Leu Leu Ala  
 225 230 235 240  
 Gly Asn Gln Pro Arg Arg Gly Glu Arg Thr Arg Ala Ile Val Val Glu  
 245 250 255  
 Ala Glu Arg Glu His Arg Glu Thr Thr Ala His Asp Gly Arg Pro Val  
 260 265 270  
 Leu Val Val Ala Arg Thr Thr Ala Ala Leu Arg Ala Gln Ile Ala Glu  
 275 280 285  
 Leu Leu Glu Arg Pro Asp Ala Asp Leu Ala Gly Val Gly Leu Gly Leu  
 290 295 300  
 Thr Thr Ala Arg His Glu His Ala Val Val Ala Ser Thr Arg Glu Glu  
 305 310 315 320  
 Ala Val Arg Gly Arg Glu Ile Ala Ala Ala Thr Ala Asp Ala Val Val  
 325 330 335  
 Glu Gly Val Thr Glu Val Asp Gly Arg Asn Val Val Phe Leu Ser Ala  
 340 345 350  
 Gly Ala Glu Ser Ser Ser Pro Gly Lys Ile Arg Ala Asp Glu Ser Met  
 355 360 365  
 Ala Pro Met Gln Asp Trp Lys Val Ser Asp Val Leu Arg Gln Ala Pro  
 370 375 380  
 Gly Ala Pro Gly Leu Asp Asp Val Val Leu Val Met Val Glu Leu Arg  
 385 390 395 400  
 Ser Tyr Val Glu Ala Val Gln Ile His Ala Ala Leu Thr Leu Glu Asp  
 405 410 415  
 Ala Ala Lys Ile Val Val Gly Arg Ser Arg Ile Met Arg Ser Leu Ser  
 420 425 430  
 Gly Glu Gly Gly Ala Ala Val Ala Leu Gly Glu Ala Ala Val Arg Glu  
 435 440 445  
 Arg Leu Arg Pro Trp Gln Asp Arg Leu Ser Val Ala Gly Arg Ser Val  
 450 455 460  
 Val Val Ser Glu Pro Gly Ala Leu Arg Ala Phe Ser Glu Asp Cys Ala  
 465 470 475 480  
 Ala Glu Gly Ile Arg Val Arg Asp Ile Asp Asp Tyr Ser Ser Pro Gln  
 485 490 495  
 Ile Glu Arg Val Arg Glu Glu Leu Leu Glu Thr Thr Gly Asp Ile Ala  
 500 505 510  
 Pro Arg Pro Ala Arg Val Pro Phe His Thr Val Glu Ser Arg Ser Met  
 515 520 525  
 Asp Gly Thr Glu Leu Asp Ala Arg Tyr Arg Asn Ile Glu Thr Arg Ala  
 530 535 540  
 Asp Val Thr Arg Leu Ala Glu Ser Tyr Asp Ala Ile Val Pro Val Val  
 545 550 555 560  
 Val Gln Ala Val Glu Glu Gln Val Glu Glu Ala Asp Gly Ala Glu Asp  
 565 570 575  
 Ala Val Val Val Gly Ser His Asp Gly Gly Asp Leu Ser Ala Phe Leu  
 580 585 590  
 Arg Ser Met Ala Thr His Val Ser Asp Ile Arg Trp Asp Val Ala Leu  
 595 600 605  
 Pro Gly Ala Ala Pro Phe Ala Thr Gln Arg Lys Tyr Leu Gln Pro Ala  
 610 615 620  
 Ala Pro Ala Ala Ala Ser Glu Leu Ala Arg Val Ser Thr Pro Ile Glu  
 625 630 635 640  
 Lys Pro Glu Ser Gly Asn Leu Asp Gly Asp Trp Val Val Thr Pro Leu  
 645 650 655  
 Ile Ser Pro Glu Trp Thr Glu Met Leu Cys Glu Ala Ile Asn Ala Asn  
 660 665 670

Gly Arg Ala Leu Arg Cys Glu Val Asp Thr Ser Ala Ser A Thr Glu  
 675 680 685  
 Met Ala Gln Ala Val Ala Gln Ala Gly Thr Gly Phe Arg Gly Leu Leu  
 690 695 700  
 Leu Ser Ser Asp Glu Ser Ala Cys Arg Pro Gly Val Pro Ala Gly Ala  
 705 710 715 720  
 Val Gly Leu Leu Thr Val Gln Ala Leu Gly Asp Ala Gly Val Asp Ala  
 725 730 735  
 Pro Val Trp Cys Leu Gln Gly Arg Thr Pro Ala Asp Asp Asp Leu Ala  
 740 745 750  
 Arg Pro Ala Gln Thr Thr Ala His Phe Ala Gln Val Ala Gly Leu Leu  
 755 760 765  
 Pro Gly Arg Trp Gly Gly Val Val Leu Pro Glu Ser Val Asp Asp Ala  
 770 775 780  
 Ala Leu Arg Leu Leu Val Val Leu Arg Gly Gly Arg Ala Glu Asp  
 785 790 795 800  
 His Leu Val Asp Gly Arg Leu His Gly Arg Val Val Arg Ala Ser Leu  
 805 810 815  
 Pro Gln Ser Gly Ser Arg Ser Trp Thr His Val Val Ala Ala Ser Pro  
 820 825 830  
 Val Asp Gln Ile Val Trp Ala Asp Arg Ala Glu Arg Val Ala Gly Ala  
 835 840 845  
 Cys Pro Gly Asp Asp Leu Ala Ala Val Glu Glu Ala Ala Ser Ala Val  
 850 855 860  
 Val Cys Gln Ala Ala Ala Leu Arg Glu Ala Leu Gly Asp Glu Pro Val  
 865 870 875 880  
 Thr Ala Leu Val Ala Gly Thr Leu Thr Asn Phe Gly Ser Ile Ser Glu  
 885 890 895  
 Val Ala Pro Glu Glu Phe Ala Glu Thr Ile Ala Ala Thr Ala Leu Leu  
 900 905 910  
 Ala Val Asp Val Leu Gly Asp Arg Ala Val Glu Arg His Val Tyr Cys  
 915 920 925  
 Val Gly Ile Trp Gly Gly Ala Gly Met Ala Ala Ala Ala Gly Ser Ala  
 930 935 940  
 Tyr Asp Ala Leu Glu His His Ala Arg Arg Ser Cys Thr Ser Val Ala  
 945 950 955 960  
 Thr Pro Leu Pro Gly Gly Ala Val Asp Asp Gly Tyr Leu Arg Glu Arg  
 965 970 975  
 Leu Arg Ser Leu Ser Ala Asp Arg Met Arg Thr Trp Glu Arg Val Ala  
 980 985 990  
 Ala Gly Pro Val Ser Val Ala Val Ala Asp Val Asp Trp Pro Val Leu  
 995 1000 1005  
 Ser Glu Gly Phe Ala Thr Arg Pro Thr Ala Leu Phe Ala Glu Leu Ala  
 1010 1015 1020  
 Gly Arg Gly Gly Gln Ala Glu Ala Glu Pro Asp Ser Gly Pro Thr Gly  
 1025 1030 1035 1040  
 Glu Pro Ala Gln Arg Leu Gly Leu Ser Pro Asp Glu Gln Gln Glu Asn  
 1045 1050 1055  
 Leu Glu Leu Val Ala Asn Ala Val Glu Val Leu His Glu Ser Ala Ala  
 1060 1065 1070  
 Glu Ile Asn Val Arg Arg Ala Ser Glu Leu Leu Asn Met Ala Lys Arg  
 1075 1080 1085  
 Leu Ser Ala Ser Thr Leu Arg Leu Pro Ala Ser Leu Val Phe Asp Thr  
 1090 1095 1100  
 Val Thr Ala Leu Gln His Leu Arg Ala Arg Val Gly Asp Ala Asp Gln  
 1105 1110 1115 1120  
 Ala Ala Val Arg Val Val Gly Ala  
 1125

<210> 39  
 <211> 1224

<212> PRT  
<213> Artificial Sequence

<220>  
<223> Alignment of the EryA SU

<400> 39  
Ala Asp Glu Ser Glu Ile Ile Gly Ile Gly Phe Gly Ile Gly Ser Glu  
1 5 10 15  
Gln Leu Arg Val Leu Ala Glu Gly Ala Asn Leu Thr Thr Gly Phe Ala  
20 25 30  
Asp Ile Gly Arg Leu Tyr His Pro Asp Pro Asp Asn Pro Gly Thr Ser  
35 40 45  
Tyr Val Asp Lys Gly Pro Leu Thr Asp Ala Asp Pro Gly Ile Thr Leu  
50 55 60  
Met Leu Met Thr Ala Ala Val Arg Ile Asp Asp Ala Arg Gly Thr Asp  
65 70 75 80  
Val Met Asn Gly Gln Ser Met Gln Leu Leu Ala Gly Glu Ala Glu Arg  
85 90 95  
Val Asp Gln Gly Ile Asn Ser Ala Ser Leu Ile Ala Thr Phe Trp Ala  
100 105 110  
Leu Thr Ser Val Gly Ile Ile Met Gln Ala Arg Gly Glu Cys Ser Leu  
115 120 125  
Leu Ala Val Thr Ser Asp Tyr Thr Phe Val Asp Ser Thr Gln Arg Gly  
130 135 140  
Ala Ser Cys Ala Ser Ala Arg Asp Ala Leu Ser Val Ala Ala Leu Val  
145 150 155 160  
Glu Pro Arg Ala Asn His Gln Ala Val Leu Arg Ser Val Gln Ala Asn  
165 170 175  
Pro Ser Glu Arg Gln Leu Ala Ala Ser Val Pro Ala Ala Val Asp Val  
180 185 190  
Glu Ile Ala Gly Ile Ala Thr Gln Asp Asp Arg Leu Arg Leu Thr Ile  
195 200 205  
Thr Ala Ala Ile Val Val Ala Met Arg His Met Leu Arg Ser His Ala  
210 215 220  
Asp Leu Ser Pro His Ile Asp Glu Ser Ala Val Glu Val Ile Arg Glu  
225 230 235 240  
Glu Val Pro Pro Ala Gly Glu Arg Pro Gly Ser Val Val Val Glu Ala  
245 250 255  
Ala Glu Gln Glu Ala Ala Arg Thr Glu Arg Gly Pro Leu Phe Val Leu  
260 265 270  
Gly Arg Ser Glu Ala Val Val Ala Arg Ala Leu Ala Glu His Leu Arg  
275 280 285  
Asp Thr Pro Glu Leu Gly Leu Thr Asp Ala Ala Trp Thr Leu Thr Gly  
290 295 300  
Ala Arg Phe Asp Val Ala Val Gly Asp Asp Arg Ala Gly Val Cys Ala  
305 310 315 320  
Glu Asp Ala Leu Glu Arg Pro Ser Ala Asp Ala Val Ala Pro Val Thr  
325 330 335  
Ser Ala Pro Arg Lys Pro Val Leu Val Ala Val Ala Arg Asp Glu Ser  
340 345 350  
Ser Glu Glu Ser Met Ser Arg Ala Glu Ala Leu Ser Pro His Thr Asp  
355 360 365  
Trp Lys Leu Leu Asp Val Val Arg Gly Asp Gly Gly Pro Asp Pro His  
370 375 380  
Glu Asp Ile Val Leu Ser Ile Met Val Glu Leu Arg Ala His Val Thr  
385 390 395 400  
Ala Val Gln Ile His Ala Ala Leu Ser Leu Glu Ala Ala Ala Lys Val  
405 410 415  
Val Ala Leu Arg Ser Gln Val Leu Arg Glu Leu Asp Asp Gln Gly Gly  
420 425 430  
Val Ser Val Gly Ala Ser Arg Asp Glu Leu Glu Thr Val Leu Ala Arg

435	440	445
Trp Asp Gly Arg Val Ala Val	Ala Gly Gly Thr Ser Val	Val Ala Pro
450	455	460
Thr Ala Glu Leu Asp Glu Phe	Phe Ala Glu Ala Glu Ala Arg	Glu Met
465	470	475
Lys Pro Arg Arg Ile Ala Arg	Tyr Ser Ser Pro Glu Val Ala Arg	Ile
485	490	495
Glu Asp Arg Ile Ala Ala Glu	Leu Gly Thr Ile Thr Ala Val Arg	Gly
500	505	510
Ser Val Pro Leu His Thr Val	Thr Gly Glu Val Ile Asp Thr	Ser Ala
515	520	525
Met Asp Ala Ser Tyr Arg Asn	Ile Arg Pro Leu Glu Gln Val Arg	Gly
530	535	540
Leu Val Glu Gln Phe Asp	Thr Val Val Pro Val Leu Leu Met	Ala Val
545	550	555
Glu Glu Thr Ala Glu His Ala	Gly Ala Glu Val Thr Cys Val Pro	Thr
565	570	575
Arg Glu Gln Ser Gly Pro His	Glu Phe Leu Arg Asn Leu Leu Arg	His
580	585	590
Val His Gly Ala Asp Leu Arg	Pro Ala Val Ala Gly Gly Arg	Pro Ala
595	600	605
Glu Thr Glu His Gln Phe Pro	Arg Pro His Arg Pro Ala Asp	Val Ser
610	615	620
Ala Leu Tyr Gly Leu Ala Glu	Gln Gly Glu Tyr Gly Pro Ser	Phe Gln
625	630	635
Ala Leu Arg Ala Ala Arg Lys	Asp Asp Ser Val Tyr Ala Glu Val	Ser
645	650	655
Ile Ala Ala Asp Glu Glu	Gly Tyr Ala Phe His Pro Val Leu Asp	Ala
660	665	670
Val Ala Gln Thr Leu Ser	Leu Gly Ala Leu Gly Glu Pro	Gly Gly
675	680	685
Lys Leu Pro Phe Ala Trp Asn	Thr Val Thr Leu His Ala Ser	Ala Thr
690	695	700
Ser Val Arg Val Val Ala Thr	Pro Ala Gly Ala Asp Ala Met	Ala Leu
705	710	715
Arg Val Thr Asp Pro Ala Gly	His Leu Val Ala Thr Asp Leu Val	Val
725	730	735
Arg Ser Thr Gly Glu Lys Trp	Glu Gln Pro Glu Pro Arg Gly	Gly Glu
740	745	750
Gly Glu Leu His Ala Asp Trp	Gly Arg Leu Ala Glu Pro Gly	Ser Thr
755	760	765
Gly Arg Val Val Ala Ala Asp	Ala Ser Asp Leu Asp Ala Val	Leu Arg
770	775	780
Ser Gly Glu Pro Glu Pro Asp	Ala Val Leu Val Arg Tyr Glu Pro	Glu
785	790	795
Gly Asp Asp Pro Arg Ala Ala	Ala Arg His Gly Val Leu Trp Ala	Ala
805	810	815
Ala Leu Val Arg Arg Trp	Leu Glu Gln Glu Leu Pro Gly	Ala Thr
820	825	830
Leu Val Ile Ala Ser Gly	Thr Val Ser Asp Asp Ser Val	Pro Glu
835	840	845
Pro Gly Ala Ala Ala Met	Trp Val Ile Arg Cys Ala Gln	Ala Ser Pro
850	855	860
Asp Arg Phe Val Leu Leu	Thr Asp Ala Glu Pro Gly Met	Leu Pro Val
865	870	875
Pro Asp Asn Pro Gln Leu	Leu Gly Asp Asp Val Phe Val	Pro Leu Ser
885	890	895
Pro Leu Ala Pro Ser Ala	Thr Gln Pro Ala Pro Val Asp	Asp Val Ile
900	905	910
Gly Thr Gly Thr Leu Arg	Leu Leu Ala His Val Thr His	Glu Val Arg
915	920	925
His Leu Val Ser Arg Arg	Gly Ala Asp Ala Pro Gly	Ser Asp Glu Arg

930	935	940	
Ala Glu Ile Glu Asp Ile	Ala Ser Ala Glu Ile	Ala Cys Thr Ala Asp	
945	950	955	960
Arg Asp Ala Leu Ser Ala Leu Leu Asp Gly	Leu Pro Arg Pro Leu Thr		
965	970	975	
Gly Val Val Ala Ala Gly Val Leu Ala Asp Gly	Leu Val Thr Ser Ile		
980	985	990	
Asp Glu Pro Ala Val Glu Gln Val Leu Arg Ala	Val Asp Ala Ala Trp		
995	1000	1005	
Asn His Leu Thr Ala Asn Thr Gly Leu Ser Phe	His Val Leu Phe Ala		
1010	1015	1020	
Ser Val Leu Ala Gly Pro Gly Gln Gly Val Ala	Ala Ala Asn Glu Ser		
1025	1030	1035	1040
Asn Ala Leu Ala Leu Arg Thr Arg Leu Pro Ala	Lys Ala Leu Gly Gly		
1045	1050	1055	
Leu Gln Ala Ser Glu Met Thr Ser Gly Leu Gly	Asp Arg Ile Ala Arg		
1060	1065	1070	
Thr Val Ala Ala Leu Pro Thr Glu Arg Leu Ala	Leu Phe Asp Ser Ala		
1075	1080	1085	
Arg Arg Gly Gly Glu Val Val Phe Pro Leu Ser	Ile Asn Arg Ser Ala		
1090	1095	1100	
Leu Arg Arg Glu Phe Val Pro Glu Val Leu Arg	Gly Met Val Arg Ala		
1105	1110	1115	1120
Lys Leu Arg Ala Ala Gly Gln Ala Glu Ala	Ala Gly Pro Asn Val Val		
1125	1130	1135	
Asp Arg Leu Gly Arg Ser Glu Ser Asp Gln Val	Ala Gly Ala Glu Leu		
1140	1145	1150	
Val Arg Ser His Ala Ala Val Ser Tyr Gly Ser	Ala Asp Gln Leu Pro		
1155	1160	1165	
Glu Arg Lys Ala Lys Asp Phe Leu Ala Val	Glu Asn Arg Leu Gly Thr		
1170	1175	1180	
Ala Thr Val Arg Leu Pro Ser Thr Leu Val	Phe Asp Thr Pro Leu Ala		
1185	1190	1195	1200
Val Glu His Leu Arg Asp Arg Phe Ala Ala	Ser Pro Ala Val Asp Ile		
1205	1210	1215	
Gly Asp Arg Leu Asp Glu Leu Glu			
1220			

<210> 40  
 <211> 1118  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Alignment of the EryA SU

<400> 40															
His	Arg	Ala	Gly	Glu	Ile	Ile	Gly	Met	Ala	Phe	Asp	Val	Asp	Ser	Glu
1				5			10				15				
Ser	Phe	Glu	Phe	Val	Ser	Gly	Gly	Gly	Asp	Ala	Ile	Ala	Glu	Ala	Ala
	20				25			30							
Glu	Pro	Asp	Pro	Asp	Ala	Arg	Leu	Gly	Met	Leu	Ala	Ala	Gly	Asp	Ala
	35				40			45							
Gly	Ile	Ser	Leu	Met	Ile	Met	Ile	Ser	Ala	Leu	Arg	His	Asp	Val	Ser
	50				55			60							
Arg	Gly	Ser	Ala	Ile	Val	Gly	Thr	Val	Asp	Gly	Pro	Arg	Pro	Asp	Glu
65					70			75			80				
Ala	Pro	Asp	Glu	Val	Leu	Val	Gly	Thr	Thr	Ala	Ser	Ser	Ala	Val	Ala
				85			90			95					
Cys	Leu	Leu	Ala	Met	Thr	Gly	Thr	Ala	Leu	Ile	Met	Glu	Ser	Arg	Asp
				100			105			110					

Glu Cys Gly Leu Ile Ala Val Thr Ser Ser Gly Ala Phe Ile Glu Arg  
 115 120 125  
 Ser Gln Gly Gly Ala Ala Cys Pro Ser Lys Ala Asp Gly Leu Ala Ala  
 130 135 140  
 Gly Val Leu Val Gln Arg Ala Arg Glu Arg Pro Ala Val Leu Arg Ser  
 145 150 155 160  
 Val Gln Thr Ser Pro Ala Gln Arg Arg Leu Glu Asn Ala Val Arg Ala  
 165 170 175  
 Gly Val Asp Tyr Arg Ile Val His Leu Ser Thr Ala Glu Asp Pro Asp  
 180 185 190  
 Asp Leu Trp Ile Ser Ile Thr Val Ala Met Ala Val Ala Leu Arg His  
 195 200 205  
 Glu Met Arg Thr His Phe Asp Pro Ser Pro Gln Ile Glu Asp Leu Ala  
 210 215 220  
 Val Ser Val Val Ser Gln Ala Arg Ser Pro Ala Gly Glu Arg Pro Gly  
 225 230 235 240  
 Ser Ile Val Val Glu Ala Glu Ala Asp Glu Pro Glu Pro Ala Pro Asp  
 245 250 255  
 Ser Gly Pro Val Leu Val Leu Gly Arg Asp Glu Gln Ala Met Arg Gly  
 260 265 270  
 Arg Leu Ala Asp His Leu Ala Arg Glu Pro Arg Asn Ser Leu Arg Asp  
 275 280 285  
 Thr Gly Phe Thr Leu Thr Arg Ser Ala Trp Glu His Val Val Val Gly  
 290 295 300  
 Asp Arg Asp Asp Ala Leu Ala Gly Arg Ala Val Asp Arg Ile Ala Asp  
 305 310 315 320  
 Arg Thr Ala Thr Gly Gln Ala Arg Thr Arg Arg Gly Val Ala Met Val  
 325 330 335  
 Ala Gln Ala Arg Asp Arg Glu Ser Gln Asp Ser Ile Arg Asp Glu Arg  
 340 345 350  
 Ala Leu Ala Pro His Val Asp Trp Ser Leu Thr Asp Leu Leu Ser Gly  
 355 360 365  
 Ala Arg Pro Leu Asp Asp Val Ala Leu Ala Val Met Val Ala Leu Arg  
 370 375 380  
 Ser His Val Glu Ala Val Gln Ile His Ala Ala Leu Thr Leu Glu Asp  
 385 390 395 400  
 Ala Ala Lys Leu Val Ala Val Arg Ser Arg Val Leu Ala Arg Leu Gly  
 405 410 415  
 Gly Gln Gly Gly Ala Ser Phe Gly Leu Gly Thr Glu Gln Ala Ala Glu  
 420 425 430  
 Arg Ile Gly Arg Phe Ala Gly Ala Leu Ser Ile Ser Gly Arg Ser Val  
 435 440 445  
 Val Val Ala Glu Ser Gly Pro Leu Asp Glu Leu Ile Ala Glu Cys Glu  
 450 455 460  
 Ala Glu Gly Ile Thr Ala Arg Arg Ile Pro Asp Tyr Ser Ser Pro Gln  
 465 470 475 480  
 Val Glu Ser Ile Arg Glu Glu Leu Leu Thr Glu Leu Ala Gly Ile Ser  
 485 490 495  
 Pro Val Ser Ala Asp Val Ala Leu Tyr Thr Thr Gly Gln Pro Ile  
 500 505 510  
 Asp Thr Ala Thr Met Asp Thr Ala Tyr Ala Asn Leu Glu Gln Arg Gln  
 515 520 525  
 Asp Thr Arg Gln Leu Ala Glu Ala Phe Asp Ala Val Val Pro Val Leu  
 530 535 540  
 Thr Val Gly Ile Glu Ala Thr Leu Asp Ser Ala Leu Pro Ala Asp Ala  
 545 550 555 560  
 Gly Ala Cys Val Val Gly Thr Arg Asp Arg Gly Gly Leu Ala Asp Phe  
 565 570 575  
 His Thr Ala Leu Gly Glu Tyr Ala Gln Glu Val Asp Trp Ser Pro Ala  
 580 585 590  
 Phe Ala Asp Ala Arg Pro Val Glu Val Gln Arg Gln Tyr Leu Pro Ile  
 595 600 605

Pro Thr Gly Gly Arg Ala Arg Glu Asp Asp Asp Trp Arg Gln Val Val  
 610 615 620  
 Arg Glu Ala Glu Trp Glu Ser Ala Ser Leu Ala Gly Arg Val Leu Val  
 625 630 635 640  
 Thr Gly Pro Gly Val Pro Ser Glu Leu Ser Asp Ala Ile Arg Ser Gly  
 645 650 655  
 Leu Glu Gln Ser Ala Thr Val Leu Thr Cys Asp Val Glu Ser Arg Ser  
 660 665 670  
 Thr Ile Gly Thr Ala Leu Glu Ala Ala Asp Thr Asp Ala Leu Ser Thr  
 675 680 685  
 Val Leu Leu Ser Arg Asp Gly Glu Ala Val Asp Pro Ser Leu Asp Ala  
 690 695 700  
 Leu Ala Val Gln Ala Leu Gly Ala Ala Gly Val Glu Ala Pro Leu Trp  
 705 710 715 720  
 Val Leu Arg Asn Gln Val Ala Asp Gly Glu Leu Val Asp Pro Ala Gln  
 725 730 735  
 Ala Met Val Gly Leu Gly Arg Val Val Gly Ile Gln Pro Gly Arg Trp  
 740 745 750  
 Gly Gly Leu Val Leu Val Asp Ala Asp Ala Ala Ser Ile Arg Ser Leu  
 755 760 765  
 Ala Val Leu Ala Asp Pro Arg Gly Glu Glu Gln Val Ile Ala Asp Gly  
 770 775 780  
 Ile Lys Val Ala Leu Val Pro Ala Pro Ala Arg Ala Ala Arg Thr Arg  
 785 790 795 800  
 Trp Ser Arg Val Val Gly Thr Gly Gly Ile Ala His Val Ala Trp Ala  
 805 810 815  
 Arg Ser Ala Glu His Val Leu Gly Arg Arg Gly Ala Asp Ala Pro Gly  
 820 825 830  
 Ala Ser Glu Arg Glu Glu Leu Thr Ala Leu Thr Gly Val Thr Ile Ala  
 835 840 845  
 Cys Val Ala Asp Arg Ala Arg Leu Glu Ala Val Leu Ala Ala Glu Arg  
 850 855 860  
 Ala Glu Gly Arg Thr Val Ser Ala Val Met Ala Ala Gly Val Ser Thr  
 865 870 875 880  
 Ser Thr Pro Leu Asp Asp Leu Thr Glu Ala Glu Phe Thr Glu Ile Ala  
 885 890 895  
 Asp Val Val Arg Gly Thr Val Asn Asp Leu Cys Pro Asp Leu Asp Ala  
 900 905 910  
 His Val Leu Phe Asn Gly Val Trp Gly Ser Pro Gly Leu Ala Ser Ala  
 915 920 925  
 Ala Ala Asn Ala Phe Asp Gly Phe Arg Arg Arg Ser Glu Ala Pro Val  
 930 935 940  
 Thr Ser Ile Ala Gly Leu Gly Gln Asn Met Ala Gly Asp Glu Gly Gly  
 945 950 955 960  
 Glu Tyr Leu Arg Ser Gln Leu Arg Ala Met Asp Pro Asp Arg Val Glu  
 965 970 975  
 Glu Leu His Ile Thr Asp His Gly Gln Thr Ser Val Ser Val Val Asp  
 980 985 990  
 Met Asp Arg Arg Arg Phe Val Glu Leu Phe Thr Ala Arg His Arg Pro  
 995 1000 1005  
 Leu Phe Asp Glu Ile Ala Gly Ala Arg Ala Glu Ala Arg Gln Ser Glu  
 1010 1015 1020  
 Glu Gly Pro Ala Leu Ala Gln Arg Leu Ala Leu Ser Thr Ala Glu Arg  
 1025 1030 1035 1040  
 Arg Glu His Ala His Leu Ile Arg Ala Glu Val Ala Val Leu His Gly  
 1045 1050 1055  
 Asp Asp Ala Ala Ile Asp Arg Asp Arg Ala Arg Asp Phe Met Thr Val  
 1060 1065 1070  
 Asp Asn Arg Leu Ala Ala Val Thr Val Arg Glu Ala Ala Thr Val Val  
 1075 1080 1085  
 Phe Asp Thr Ile Thr Arg Leu Asp His Tyr Leu Glu Arg Val Gly Ala  
 1090 1095 1100

Ala Glu Ala Glu Glu Ala Pro Ala Leu Val Arg Glu Val P  
1105 1110 1115

<210> 41  
<211> 1099  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Alignment of the EryA SU

<400> 41  
Lys Asp Ala Asp Asp Ile Ile Gly Met Ala Phe Gly Val His Asn Gly  
1 5 10 15  
Glu Leu Glu Phe Ile Val Gly Arg Gly Asp Ala Val Thr Glu Met Thr  
20 25 30  
Asp Leu Asp Ala Leu Phe Asp Pro Asp Pro Gln Arg His Gly Thr Ser  
35 40 45  
Tyr Ser Arg His Ala Phe Leu Asp Gly Ala Asp Ala Ala Ile Ser Leu  
50 55 60  
Met Gln Val Thr Thr Leu Phe Asn Ile Asp His Ser Arg Gly Ser Asp  
65 70 75 80  
Leu Ala Ala Tyr Gln Gly Gly Gln Asp Ala Val Val Pro Glu Asp Ser  
85 90 95  
Glu Leu Leu Thr Asn Ser Ser Ala Val Val Ala Val Leu Leu Ala Val  
100 105 110  
Thr Ser Val Ala Leu Ser Cys Gly Ser Asp Gly Asp Cys Gly Leu Val  
115 120 125  
Ala Val Ser Ala Gly Glu Val Phe Thr Glu Ser Arg Gln Gly Gly Ala  
130 135 140  
Val Cys Ala Ser Ala Glu Asp Gly Phe Ala Val Ala Val Val Leu Gln  
145 150 155 160  
Arg Asp Arg Ala Arg Gln Gly Val Val Ala Ser Leu Gln Ala Ser Val  
165 170 175  
Ala Gln Arg Lys Trp Ala Arg Ala Ile Thr Gly Ala Val Ala Val Arg  
180 185 190  
Val Ala Ser Leu Ala Thr Lys Ser Gly Ser Ser Gly Val Leu Leu Ser  
195 200 205  
Ile Ala Val Ala Ile Val Val Gly Leu Asn Arg Leu Val Pro Met Cys  
210 215 220  
Arg Gly Arg Ser Pro Leu Ile Glu Ser Ser Gly Val Glu Leu Ala Glu  
225 230 235 240  
Ala Val Ser Pro Pro Ala Ala Asp Gly Val Gly Ala Val Val Ile  
245 250 255  
Ala Pro Glu Pro Glu Pro Leu Pro Glu Pro Gly Pro Val Gly Val Leu  
260 265 270  
Ala Ala Ala Asn Ser Val Val Leu Leu Ala Arg Thr Glu Thr Ala Leu  
275 280 285  
Ala Arg Leu Leu Glu Ser Ala Val Asp Asp Ser Val Pro Leu Thr Ala  
290 295 300  
Leu Ala Ser Ala Leu Thr Gly Ala His Leu Pro Arg Ala Leu Ile Ala  
305 310 315 320  
Gly Asp His Glu Gln Leu Arg Gly Gln Arg Ala Val Glu Val Ala Ala  
325 330 335  
Pro Gly Ala Thr Thr Gly Thr Ala Ser Ala Gly Gly Val Val Phe Val  
340 345 350  
Ala Glu Ala Arg Gly Ser Val Pro Glu Ser Ile Ala Glu Asp Ala Val  
355 360 365  
Leu Ser Glu Val Ala Gly Phe Ser Ala Ser Glu Val Leu Glu Gln Arg  
370 375 380  
Pro Asp Ala Pro Ser Leu Glu Asp Val Val Leu Ser Val Met Val Arg

385	390	395	400							
Leu	Gly	Ala	Cys							
Val	Ser	Ser	Ile							
405			Gln							
Glu	Asp	Gly	Val	Arg	Val	Val	Ala	Leu	Arg	Ala
420			Leu	Arg	Ala	Lys	Ala	Leu	Arg	Ala
Leu	Ala	Gly	Arg	Gly	Gly	Val	Ser	Leu	Ala	Ala
435			Leu	Ala	Ala	Pro	Gly	Glu	Arg	Ala
Arg	Ala	Leu	Ile	Ala	Pro	Trp	Glu	Asp	Arg	Ile
450							Ser	Val	Ala	Ser
Ser	Val	Val	Val	Ser	Asp	Pro	Glu	Ala	Leu	Glu
465								Ala	Leu	Val
Cys	Glu	Asp	Glu	Gly	Val	Arg	Ala	Lys	Thr	Leu
485									Pro	Asp
Arg	His	Val	Glu	Ile	Arg	Glu	Thr	Ile	Leu	Ala
500									Asp	Gly
Ile	Ser	Ala	Arg	Arg	Ala	Ala	Ile	Pro	Leu	Tyr
515									Thr	Leu
Arg	Arg	Asp	Gly	Ala	Asp	Met	Gly	Pro	Arg	Tyr
530									Asp	Asn
Arg	Asp	Glu	Val	Ser	Ala	Ala	Val	Ala	Leu	Ser
545									Gln	
Val	Ile	Thr	Ala	Ala	Val	Gln	Glu	Ile	Ala	Ala
565									Asp	Ala
Gly	Ser	His	Asp	Thr	Ala	Glu	Glu	His	Ile	Ile
580									Ala	Glu
His	Val	His	Ala	Val	Asp	Trp	Arg	Asx	Val	Phe
595									Pro	Ala
Val	Ala	Asn	Glu	Pro	Gln	Tyr	Leu	Ala	Pro	Pro
610										
Asp	Ser	Arg	Arg	Val	Asp	Arg	Pro	Leu	Ala	Thr
625										Pro
Glu	Gly	Gly	Phe	Val	His	Gly	Ser	Ala	Pro	Glu
645										Leu
Val	Glu	Lys	Ala	Gly	Arg	Val	Val	Pro	Ala	Ser
660										Asp
Ala	Ser	Ala	Ala	Leu	Arg	Glu	Val	Pro	Gly	Glu
675										Leu
His	Thr	Gly	Ala	Ala	Thr	His	Leu	Ala	His	Gln
690										Ser
Gly	Val	Arg	Ala	Pro	Leu	Trp	Leu	Val	Ser	Leu
705										Gly
Glu	Pro	Val	Asp	Pro	Glu	Gln	Ala	Met	Arg	Gly
725									Val	Met
Gly	Leu	Thr	Pro	Glu	Arg	Trp	Gly	Gly	Leu	Val
740									Leu	Pro
Ala	Pro	Gly	Asp	Gly	Glu	Ala	Phe	Val	Cys	Leu
755										Gly
Glu	Asp	Gln	Val	Ile	Asp	His	Ala	Arg	Tyr	Gly
770										Arg
Pro	Leu	Gly	Thr	Arg	Glu	Ser	Ser	Trp	Glu	Ala
785										Ala
Ala	Leu	Gly	His	Val	Ala	His	Ala	Arg	Cys	Val
805										Glu
Arg	Arg	Gly	Val	Asp	Ala	Pro	Gly	Ala	Ala	Glu
820										Leu
Ala	Ile	Ala	Lys	Thr	Thr	Ile	Thr	Cys	Val	Ala
835										Asp
Ser	Lys	Leu	Leu	Glu	Glu	Leu	Arg	Gly	Gln	Gly
850										Arg
Val	Val	Thr	Ala	Gly	Val	Pro	Glu	Ser	Arg	Pro
865										Leu
Glu	Leu	Glu	Ser	Val	Cys	Ala	Ala	Val	Thr	Gly

885 890 895  
Cys Pro Asp Ala Glu Thr His Val Leu Phe Gly Gly Val Trp Gly Ser  
900 905 910  
Ala Asn Leu Gly Ala Ser Ala Ala Asn Ala Tyr Asp Ala Leu His Arg  
915 920 925  
Arg Ala Glu Arg Ala Ala Thr Ser Val Ala Gly Ala Gly Glu Gly Met  
930 935 940  
Ala Thr Gly Asp Leu Glu Gly Leu Thr Arg Arg Leu Arg Pro Met Ala  
945 950 955 960  
Pro Glu Arg Ile Arg Ala Leu His Gln Ala Asp Asn Gly Asp Thr Cys  
965 970 975  
Val Ser Ile Ala Asp Val Asp Trp Glu Ala Phe Ala Val Gly Phe Thr  
980 985 990  
Ala Arg Pro Arg Pro Leu Leu Asp Glu Leu Val Thr Pro Ala Val Gly  
995 1000 1005  
Ala Val Pro Ala Val Gln Ala Pro Ala Arg Glu Met Thr Ser Gln Glu  
1010 1015 1020  
Leu Glu Phe Thr His Ser His Val Ala Ile Leu His Ser Ser Pro Asp  
1025 1030 1035 1040  
Ala Val Gly Gln Asp Gln Pro Thr Glu Phe Leu Thr Val Gly Asn Gln  
1045 1050 1055  
Leu Gln Gln Ala Thr Leu Ala Leu Pro Ala Thr Leu Val Phe Glu Thr  
1060 1065 1070  
Val Arg Arg Leu Asp His Ile Gly Gln Gln Asp Ser Gly Thr Pro Ala  
1075 1080 1085  
Arg Glu Ala Ser Ser Ala Leu Arg Asp Gly Tyr  
1090 1095